A preferred derivative of ceSREBP consists of or comprises an amino acid sequence that has at least 55%, preferably at least 66%, and more preferably, at least 65% sequence identity with amino acid residues 335-428 of SEQ ID NO:2 (i.e. the bHLH-Zip domain). Other preferred derivatives of ceSREBP consist of or comprise an amino acid sequence that shares at least 75% similarity, preferably at least 80% similarity, and more preferably, at least 85% similarity with amino acid residues 335-428 of SEQ ID NO:2. Preferably, such derivatives share antigenicity with amino acid residues 335-428 of SEQ ID NO:2.

C1

IN THE CLAIMS:

A marked up version of the following claims is attached hereto as Exhibit B, wherein [bracketed text] has been deleted and underlined text has been added.

Please amend the claims as follows:

Cancel claims 5, 7, 12, 19-21, 24 and 29-33 without prejudice.

Please amend the following claims to recite as below:

1 (once amended). A *C. elegans* that has been genetically engineered to express or mis-express an SREBP pathway protein selected from the group consisting of SREBP, SCAP, and S2P, or the progeny of said *C. elegans* that has inherited said SREBP pathway protein expression or mis-expression, wherein said SREBP pathway protein expression or mis-expression results in an intestinal defect phenotype.

C2

2 (once amended). The *C. elegans* of Claim 1 that has been genetically engineered by a method selected from the group consisting of transposon insertion mutagenesis, double-stranded RNA interference, and chemical mutagenesis.

3 (once amended). The *C. elegans* of Claim 1 wherein a heterologous promoter drives expression or mis-expression of said SREBP pathway protein.

4 (once amended). The *C. elegans* of Claim 3 wherein said heterologous promoter is selected from the group consisting of tissue-specific promoters, developmental-specific promoters, and inducible promoters.

6 (once amended). The *C. elegans* of Claim 1 wherein said SREBP pathway protein is encoded by an SREBP pathway nucleic acid sequence linked to a nucleic acid sequence that encodes one or more selectable markers that allows detection of expression of said SREBP pathway protein.

C3

8 (once amended). The *C. elegans* of Claim 1 wherein said SREBP pathway protein is SREBP and comprises the amino acid sequence of SEQ ID NO:2 or a functionally-active fragment thereof.

C4

9 (once amended). The *C. elegans* of Claim 8 wherein said SREBP or functionally active fragment is encoded by the nucleic acid sequence of SEQ ID NO:1, or a fragment thereof.

10 (once amended). The *C. elegans* of Claim 1 that is heterozygous for deletion of SREBP.

11 (once amended). The *C. elegans* of Claim 1 wherein said intestinal defect phenotype is a pale intestine phenotype.

C5

13 (twice amended). A method for studying lipid metabolism comprising obtaining a first *C. elegans* defined by Claim 1 and a second *C. elegans* that has the same genetic engineering as the first *C. elegans* and that additionally has a mutation in a gene of interest, and detecting a difference between the intestinal defect phenotype of the first *C. elegans* and the intestinal defect phenotype of the second *C. elegans*, wherein a difference in the phenotypes identifies the gene of interest as capable of modifying the function of the gene encoding said SREBP pathway protein.

15 (once amended). The method of Claim 13 wherein said intestinal defect phenotype is a pale intestine phenotype.

16 (once amended). The method of Claim 13 wherein said detecting step comprises staining the first and second *C. elegans in vivo* with a fluorescently-labelled fatty acid conjugate to measure lipid content within said first and second *C. elegans*.

C6

17 (once amended). The method of Claim 16 wherein said fluorescently-labelled fatty acid conjugate comprises a fatty acid selected from the group consisting of 4,4-difluoro-5,7-dimethyl- 4-bora-3a,4a-diaza-s-indacene-3-dodecanoic acid, and 4,4-difluoro-5-methyl-4-bora-3a,4a-diaza-s-indacene-3-dodecanoic acid.

18 (once amended). A method for studying lipid metabolism comprising administering one or more compounds to a *C. elegans* defined by Claim 1; and observing any changes in lipid content of said *C. elegans*.

22 (once amended). An isolated nucleic acid molecule of less than 15 kb comprising a nucleic acid sequence that (a) hybridizes to SEQ ID NO:1 under conditions comprising hybridizing in a buffer comprising 6X SSC / 0% formamide at 34°C and washing in a buffer comprising 2X SSC at 45°C, and (b) encodes a functionally active SREBP polypeptide, said polypeptide having at least 80% sequence identity with amino

C7